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## RAW SEQUENCE LISTING

DATE: 10/21/2002

PATENT APPLICATION: US/09/997,425

TIME: 16:04:02

Input Set : A:\Cura475c.app

Output Set: N:\CRF4\10212002\I997425.raw

3 <110> APPLICANT: Edinger et al.  
 5 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
 7 <130> FILE REFERENCE: 21402-175CIP1  
 9 <140> CURRENT APPLICATION NUMBER: 09/997,425  
 10 <141> CURRENT FILING DATE: 2001-11-29  
 12 <150> PRIOR APPLICATION NUMBER: 60/242,485  
 13 <151> PRIOR FILING DATE: 2000-10-23  
 15 <150> PRIOR APPLICATION NUMBER: 60/263,339  
 16 <151> PRIOR FILING DATE: 2001-01-22  
 18 <150> PRIOR APPLICATION NUMBER: 60/264,850  
 19 <151> PRIOR FILING DATE: 2001-01-29  
 21 <150> PRIOR APPLICATION NUMBER: 10/035,568  
 22 <151> PRIOR FILING DATE: 2001-10-22  
 24 <160> NUMBER OF SEQ ID NOS: 92  
 26 <170> SOFTWARE: PatentIn Ver. 2.1  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 1747  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Homo sapiens  
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 35 ttgggaaagc tgggtgctgct gctgcctgat tcccgcgcgac agaccttggg accggggcca 120  
 36 acactggcag ctggagatgg cggacacgag atccgtgcac gagactaggt ttgaggcggc 180  
 37 cgtgaagggt atccagagtt tgccgaagaa tggttcattc cagccaacaa atgaaatgat 240  
 38 gcttaaattt tatagcttct ataagcaggc aactgaagga ccctgtaaac tttcaaggcc 300  
 39 tggatttttg gatcctattg gaagatataa atgggatgct tggagtccac tgggtgatat 360  
 40 gaccaaagag gaagccaatga ttgcataatg tgaagaaatg aaaaagatta ttgaaactat 420  
 41 gccaatgact gagaaagtgg aagaattgct gcgtgtcata ggtccatttt atgaaattgt 480  
 42 cgaggacaaa aagagtggca ggagtcttga tataacctca gatcttggtg atgttctcac 540  
 43 ttctgctccg aacgccaaaa ccgttaatgg taaagctgaa agcagtgaca gtggagccga 600  
 44 gtctgaggaa gaagaggccc aagaagaagt gaaaggagca gaacaaagtg ataatgataa 660  
 45 gaaaatgatg aagaagtcag cagaccataa gaatttgga gtcattgtca ctaatggcta 720  
 46 tgataaagat ggctttgttc aggatataca gaatgacatt catgccagtt cttccctgaa 780  
 47 tggcagaagc actgaagaag taaagcccat tgatgaaaac ttggggcaaa ctggaaaatc 840  
 48 tgctgtttgc attcaccaag atataaatga tgatcatgtt gaagatgtta caggaaattca 900  
 49 gcatttgaca agcgattcag acagtgaagt ttactgtgat tctatggaac aatttggaac 960  
 50 agaagagtct ttagacagct ttacgtccaa caatggacca tttcagtatt acttgggtgg 1020  
 51 tcattccagt caacccatgg aaaattctgg atttcgtgaa gatattcaag tacctcctgg 1080  
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 53 tggaggagaa gatggcagga ataacagcgg agcaccacac cgggagaagc gaggcggaga 1200  
 54 aactgacgaa ttctctaatt ttagaagagg aagaggacat aggatacaac acttgagcga 1260  
 55 aggaaccaag ggccggcagg tgggaagtgg aggtgatggg gagcgctggg gctccgacag 1320  
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ENTERED

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57 catgcagaat gtccttcaga gactgcagaa actggaaacg ctgactgctt tgcaggcaaa 1440
58 atcatcaaca tcaacattgc agactgctcc tcagcccacc tcacagagac catcttggtg 1500
59 gcccttcgag atgtctcctg gtgtgctaac gtttgccatc atatggcctt ttattgcaca 1560
60 gtggttggtg tatttatact atcaaagaag gagaagaaaa ctgaactgag gaaaatggtg 1620
61 ttttcctcaa gaagactact ggaactggat gacctcagaa tgaactggat tgtggtgttc 1680
62 acaagaaaat cttagtttgt gatgattaca ttgctttttg ttgtccagta gtttagtttg 1740
63 tgtacat 1747
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67 <211> LENGTH: 523
68 <212> TYPE: PRT
69 <213> ORGANISM: Homo sapiens
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73 1 5 10 15
75 Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu
76 20 25 30
78 Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
79 35 40 45
81 Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr
82 50 55 60
84 Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
85 65 70 75 80
87 Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
88 85 90 95
90 Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
91 100 105 110
93 Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
94 115 120 125
96 Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
97 130 135 140
99 Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr
100 145 150 155 160
102 Ser Asp Leu Gly Asn Val Leu Thr Ser Ala Pro Asn Ala Lys Thr Val
103 165 170 175
105 Asn Gly Lys Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu
106 180 185 190
108 Glu Ala Gln Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys
109 195 200 205
111 Lys Met Met Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val
112 210 215 220
114 Thr Asn Gly Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp
115 225 230 235 240
117 Ile His Ala Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys
118 245 250 255
120 Pro Ile Asp Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile
121 260 265 270
123 His Gln Asp Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln
124 275 280 285
126 His Leu Thr Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu

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Input Set : A:\Cura475c.app

Output Set: N:\CRF4\10212002\I997425.raw

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127      290      295      300
129 Gln Phe Gly Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly
130 305      310      315      320
132 Pro Phe Gln Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn
133      325      330      335
135 Ser Gly Phe Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile
136      340      345      350
138 Gly Asn Met Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His
139      355      360      365
141 Gly Gly Glu Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys
142      370      375      380
144 Arg Gly Gly Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly
145 385      390      395      400
147 His Arg Ile Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly
148      405      410      415
150 Ser Gly Gly Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly
151      420      425      430
153 Ser Leu Asn Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp
154      435      440      445
156 Met Gln Asn Val Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala
157      450      455      460
159 Leu Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro
160 465      470      475      480
162 Thr Ser Gln Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val
163      485      490      495
165 Leu Thr Phe Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr
166      500      505      510
168 Leu Tyr Tyr Gln Arg Arg Arg Arg Lys Leu Asn
169      515      520

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172 &lt;210&gt; SEQ ID NO: 3

173 &lt;211&gt; LENGTH: 534

174 &lt;212&gt; TYPE: PRT

175 &lt;213&gt; ORGANISM: Homo sapiens

177 &lt;220&gt; FEATURE:

178 &lt;221&gt; NAME/KEY: VARIANT

179 &lt;222&gt; LOCATION: (3)

180 <223> OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the  
181 specification

183 &lt;400&gt; SEQUENCE: 3

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W--> 184 Met Tyr Xaa Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys
185 1      5      10      15
187 Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu
188      20      25      30
190 Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
191      35      40      45
193 Val Lys Val Ile Gln Ser Leu Pro Lys Asn Asp Ser Phe Gln Pro Thr
194      50      55      60
196 Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
197 65      70      75      80

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Input Set : A:\Cura475c.app

Output Set: N:\CRF4\10212002\I997425.raw

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199 Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
200      85      90      95
202 Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
203      100      105      110
205 Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
206      115      120      125
208 Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
209      130      135      140
211 Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr
212 145      150      155      160
214 Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn
215      165      170      175
217 Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu
218      180      185      190
220 Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu
221      195      200      205
223 Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys
224      210      215      220
226 Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp
227 225      230      235      240
229 Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser
230      245      250      255
232 Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu Asn
233      260      265      270
235 Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp Ile Asn
236      275      280      285
238 Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr Ser Asp
239      290      295      300
241 Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln Glu
242 305      310      315      320
244 Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr Tyr
245      325      330      335
247 Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg Glu
248      340      345      350
250 Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln Val
251      355      360      365
253 Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu Asp Gly
254      370      375      380
256 Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu Thr
257 385      390      395      400
259 Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln His
260      405      410      415
262 Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp Gly
263      420      425      430
265 Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu Gln
266      435      440      445
268 Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn Val Leu
269      450      455      460
271 Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala Lys Ser

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Input Set : A:\Cura475c.app

Output Set: N:\CRF4\10212002\I997425.raw

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272 465          470          475          480
274 Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg Pro
275          485          490          495
277 Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala Ile
278          500          505          510
280 Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr Gln Arg
281          515          520          525
283 Arg Arg Arg Lys Leu Asn
284          530
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 536
289 <212> TYPE: PRT
290 <213> ORGANISM: Homo sapiens
292 <400> SEQUENCE: 4
293 Met Leu Phe Leu Ser Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys
294 1          5          10          15
296 Cys Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp
297          20          25          30
299 Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu
300          35          40          45
302 Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln
303          50          55          60
305 Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala
306 65          70          75          80
308 Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile
309          85          90          95
311 Gly Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys
312          100          105          110
314 Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu
315          115          120          125
317 Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly
318          130          135          140
320 Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp
321 145          150          155          160
323 Ile Thr Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu
324          165          170          175
326 Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys
327          180          185          190
329 Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln
330          195          200          205
332 Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met
333          210          215          220
335 Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly
336 225          230          235          240
338 Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala
339          245          250          255
341 Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp
342          260          265          270
344 Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/997,425

DATE: 10/21/2002  
TIME: 16:04:03

Input Set : A:\Cura475c.app  
Output Set: N:\CRF4\10212002\I997425.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 3